



FIG. 1

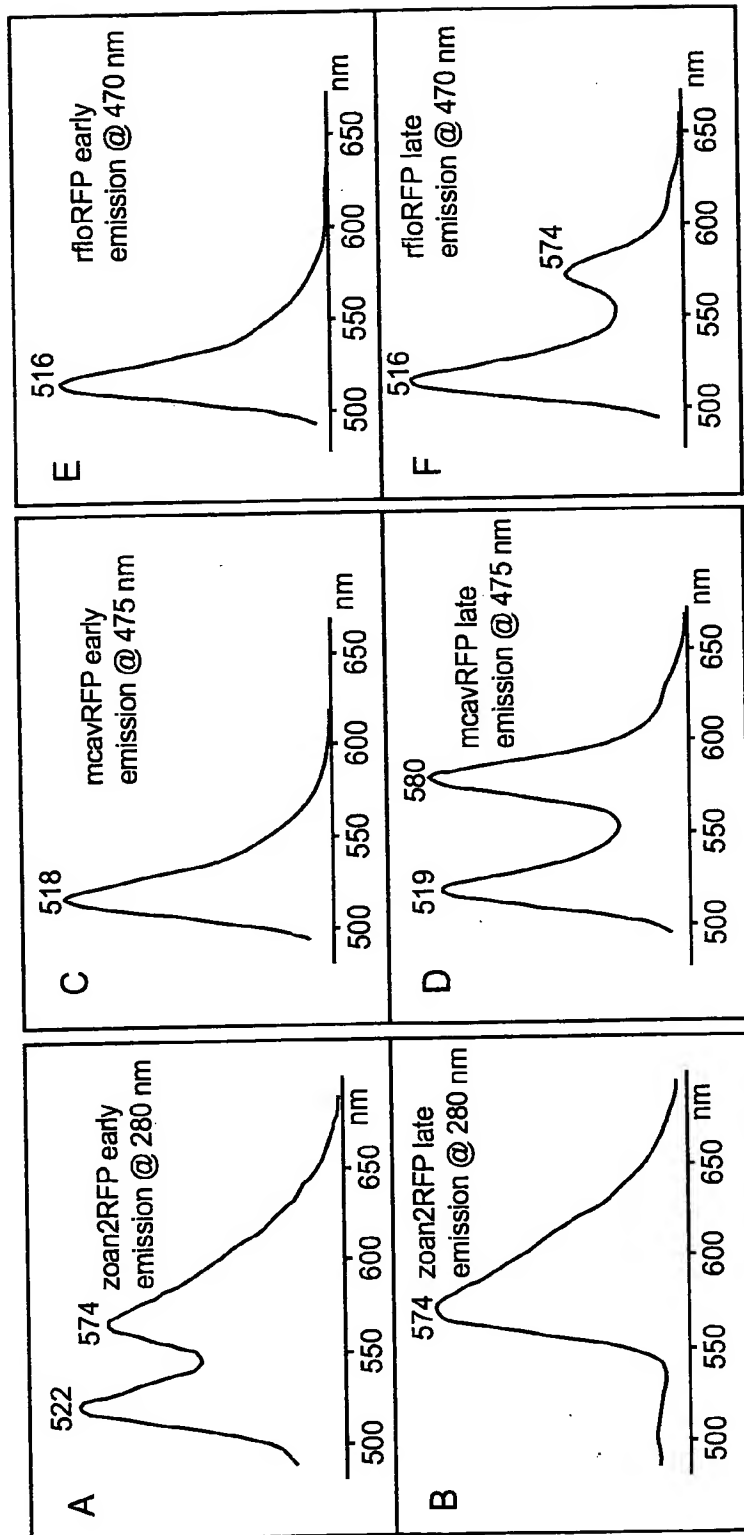


FIG. 2

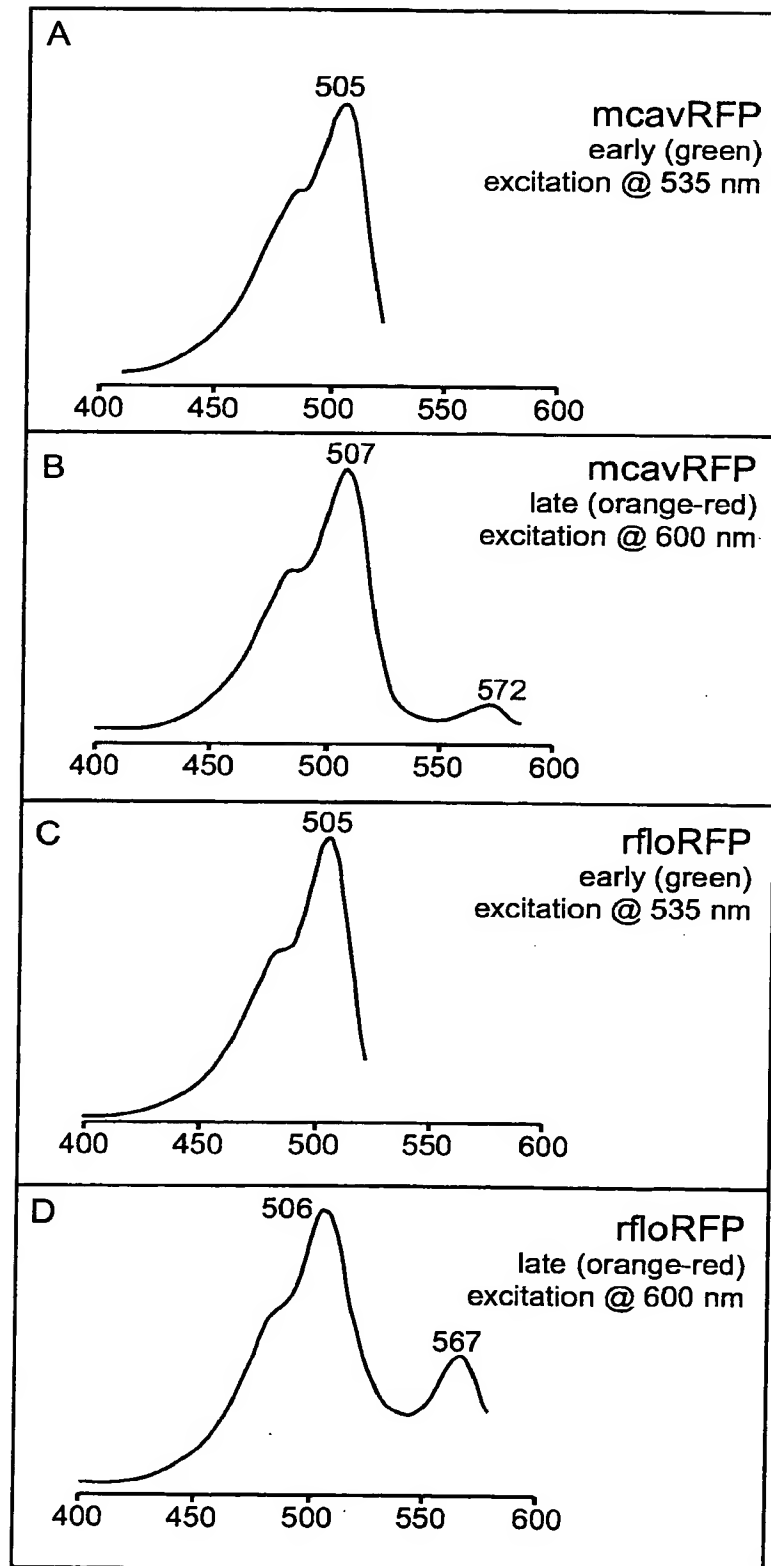


FIG. 3

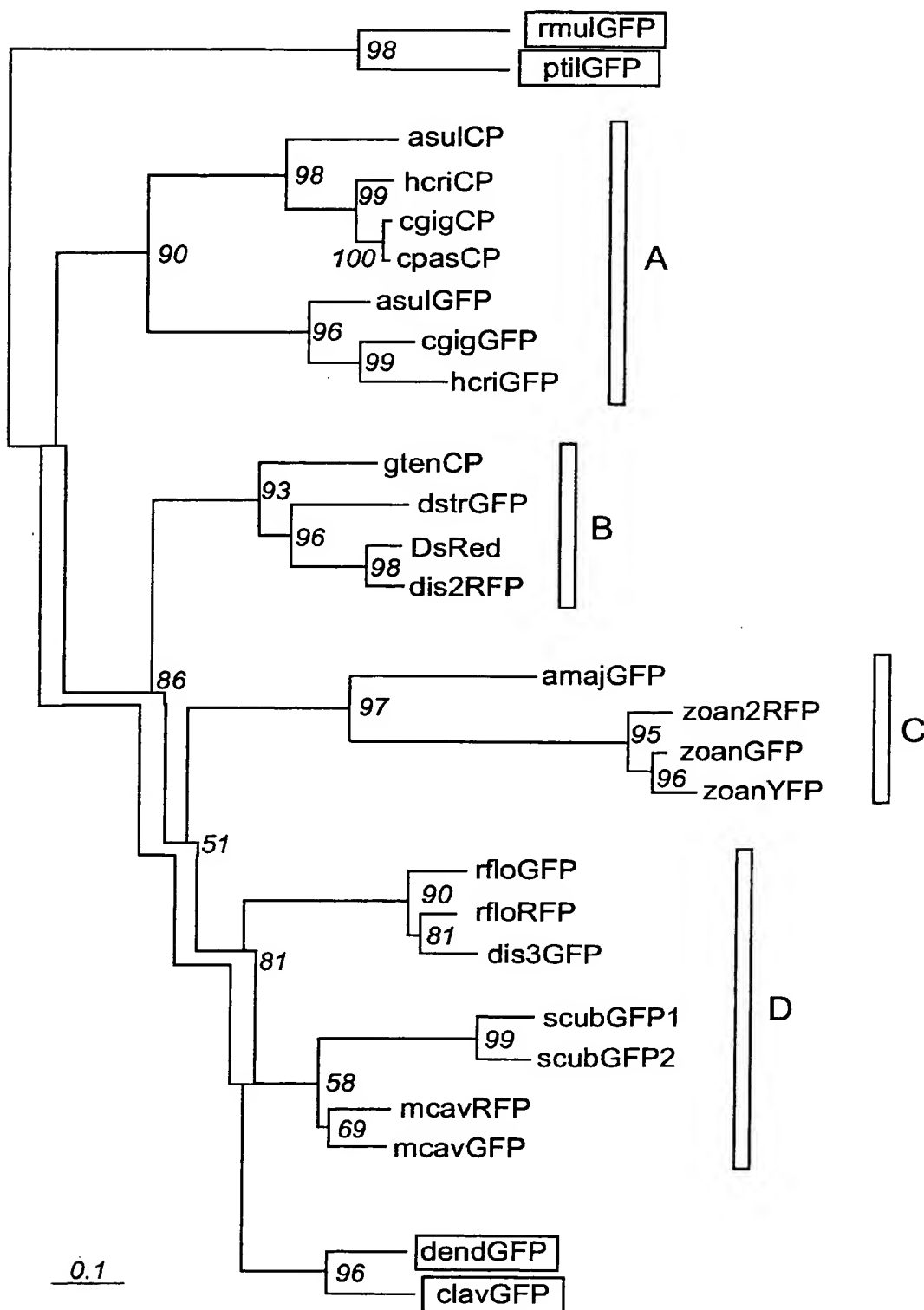


FIG. 4A

Protein ID (original ID)	GenBank accession #	Reference
amajGFP (amFP486) dstrGFP (dsFP483) clavGFP (cFP484)	AF168421 AF168420 AF168424	2 2 2
GFP cgigGFP hcriGFP	M62653 AY037776 AF420592	34 this paper this paper
ptilGFP mulGFP zoanGFP (zFP506) asulGFP (asFP499) dis3GFP dendGFP mcavGFP rloGFP scubGFP1 scubGFP2	AY015995 AY015996 AF168422 AF322221 AF420593 AF420591 AY037769 AY037772 AY037767 AY037771	35 35 2 4 this paper this paper this paper this paper this paper this paper
zoanYFP (zFP538)	AF168423	2
DsRed (drFP583) dis2RFP (dsFP593) zoan2RFP	AF168419 AF272711 AY059642	2 36 this paper
mcavRFP rloRFP	AY037770 AY037773	this paper this paper
asulCP (asCP)	AF246709	3, 4
hcriCP (hcCP) cgigCP (cgCP) cpasCP (cgCP) gtenCP (gtCP)	AF363776 AF363775 AF383155 AF383156	5 5 5 5

FIG. 4B

Taxonomy <i>Genus species</i> (Class, Sub-class, Order)
<i>Anemonia majano</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma striata</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Clavularia sp.</i> (Anthozoa, Alcyonaria, Alcyonacea)
<i>Aequorea victoria</i> (Hydrozoa,....., Hydroida) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Heteractis crispa</i> (Anthozoa, Zoantharia, Actiniaria)
<i>Ptilosarcus sp.</i> (Anthozoa, Alcyonaria, Pennatulacea) <i>Renilla muelleri</i> (Anthozoa, Alcyonaria, Pennatulacea) <i>Zoanthus sp.</i> (Anthozoa, Alcyonaria, Zoanthidea) <i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma sp.3</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Dendronephthya sp.</i> (Anthozoa, Alcyonaria, Alcyonacea) <i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordea florida</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia)
<i>Zoanthus sp.</i> (Anthozoa, Zoantharia, Zoanthidea)
<i>Discosoma sp.1</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Discosoma sp.2</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Zoanthus sp.2</i> (Anthozoa, Zoantharia, Zoanthidea)
<i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordea florida</i> (Anthozoa, Zoantharia, Corallimorpharia)
<i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria)
<i>Heteractis crispa</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis passiflora</i> (Anthozoa, Zoantharia, Actiniaria) <i>Goniopora tenuidens</i> (Anthozoa, Zoantharia, Scleractinia)

FIG. 4C

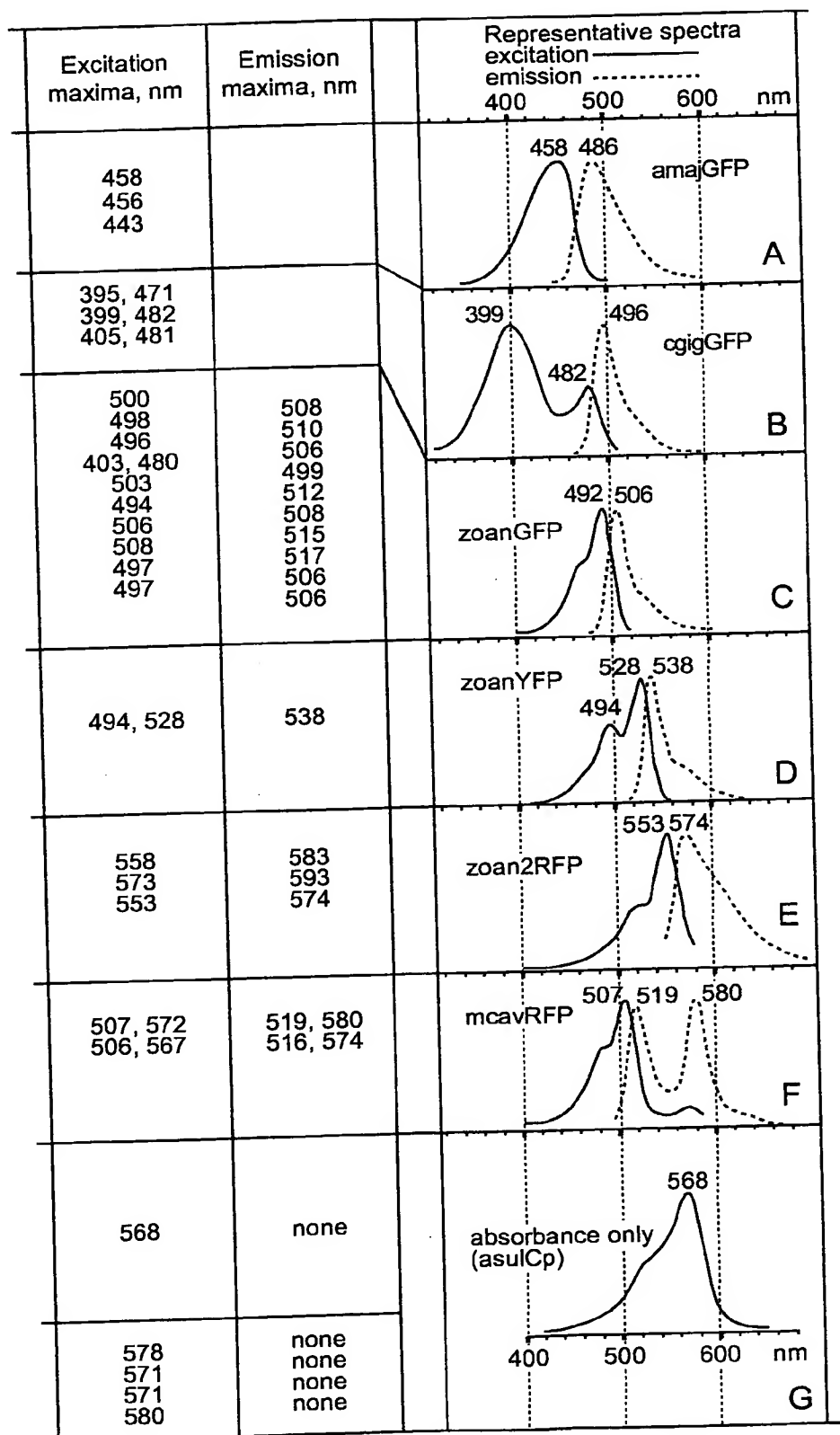


FIG. 4D

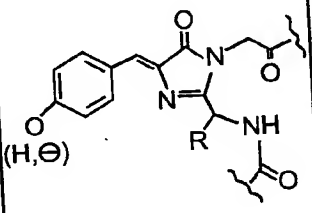
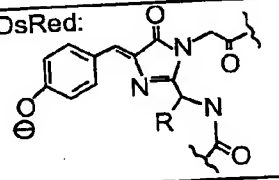
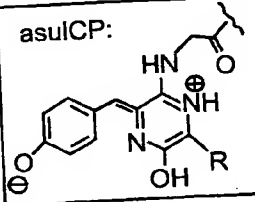
color	Representative chromophore structure
GREEN	<p>GFP:</p> 
YELLOW	?
ORANGE-RED	<p>DsRed:</p> 
	?
PURPLE-BLUE	<p>asulCP:</p> 
	?

FIG. 5

Table 2

clade	colors	Zoantharia orders
A	Green, purple-blue	Actiniaria
B	Green, orange-red, purple-blue	Corallimorpharia, Scleractinia
C	Green, yellow, orange-red	Actiniaria, Zoanthidea
D	Green, orange-red	Corallimorpharia, Scleractinia

FIG. 6

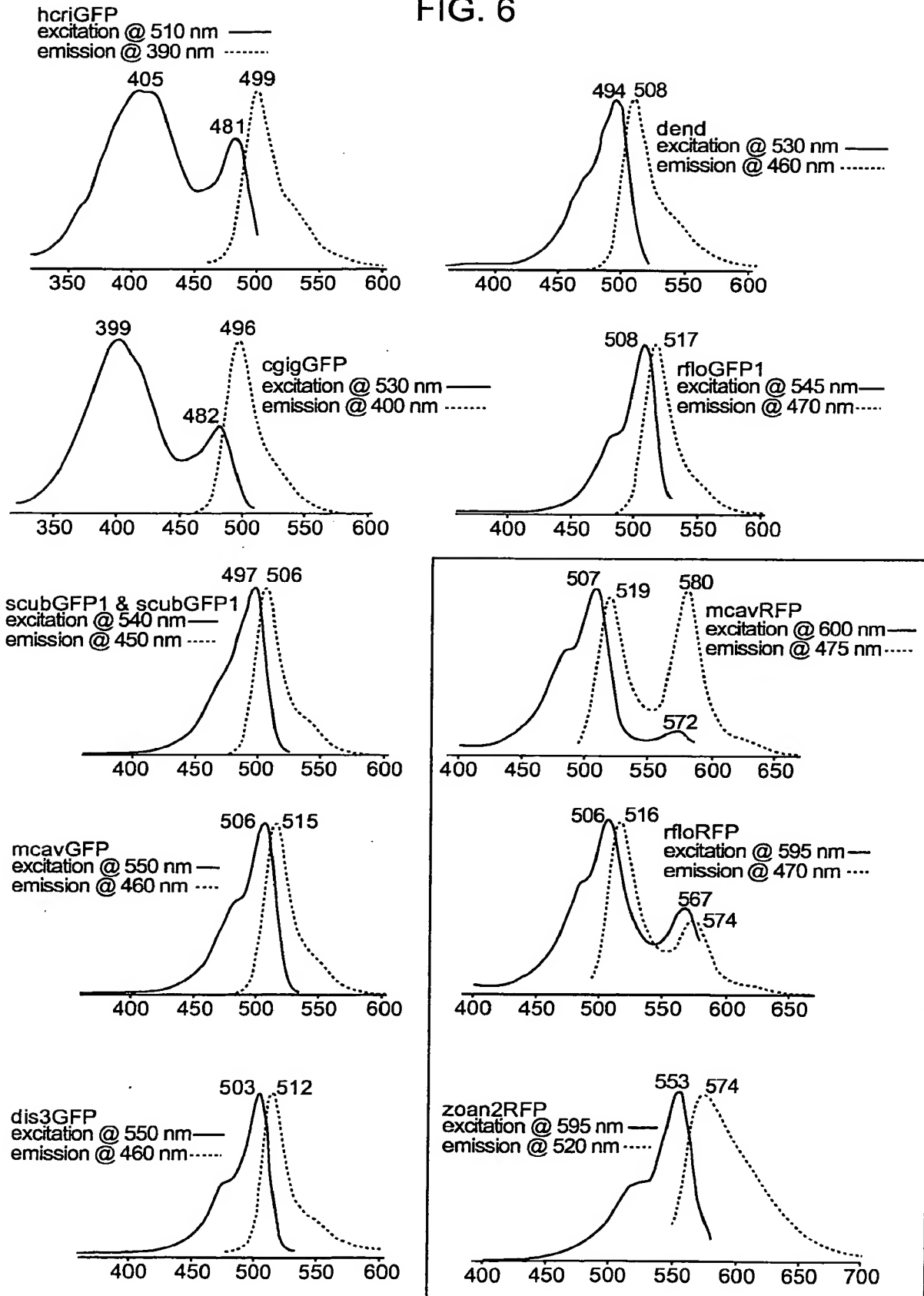


FIG. 7A

	10	20	30	40	50	60	
GFP	-----	-----	-----	-----	-----	-----	
rmulGFP	-----	-----	-----	-----	-----	-----	67
pt1lGFP	-----	-----	-----	-----	-----	-----	71
asulGFP	-----	-----	-----	-----	-----	-----	71
hcriCP	-----	-----	-----	-----	-----	-----	65
cgigCP	-----	-----	-----	-----	-----	-----	65
cpasCP	-----	-----	-----	-----	-----	-----	65
asulGFP	-----	-----	-----	-----	-----	-----	65
cgigGFP	-----	-----	-----	-----	-----	-----	65
hcriGFP	-----	-----	-----	-----	-----	-----	65
aasp?FP	-----	-----	-----	-----	-----	-----	65
gtenCP	-----	-----	-----	-----	-----	-----	63
dstrGFP	-----	-----	-----	-----	-----	-----	64
DeRed	-----	-----	-----	-----	-----	-----	68
dis2RFP	-----	-----	-----	-----	-----	-----	68
amajGFP	-----	-----	-----	-----	-----	-----	68
zoanGFP	-----	-----	-----	-----	-----	-----	70
zoanYFP	-----	-----	-----	-----	-----	-----	68
zoan2RFP	-----	-----	-----	-----	-----	-----	68
rf1orFP	-----	-----	-----	-----	-----	-----	64
rf1oGFP	-----	-----	-----	-----	-----	-----	64
dis3GFP	-----	-----	-----	-----	-----	-----	68
scubGFP1	-----	-----	-----	-----	-----	-----	70
scubGFP2	-----	-----	-----	-----	-----	-----	64
ncavRFP	-----	-----	-----	-----	-----	-----	64
ncavGFP	-----	-----	-----	-----	-----	-----	71
dendGFP	-----	-----	-----	-----	-----	-----	64
clavGFP	-----	-----	-----	-----	-----	-----	106

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70 80 90 100 110 120 130 140 150 160 169

GFp : VQFSRYPDHMKQHDFFKSAM---PEGVQERTIFYKDDGNYKRAEVKFGD---TVNRIELKGDIFKEDGNILGHKMEYNNSHVYTNADKQNGIKVNFKIRH : 169

irmulGFp : NRTFTKYPNDIS--DYFIQSF---PAGFWERILRYEDGGLVEIRSDINLIED---KFVVRVEYKGSNFPDDGPVM--QKTIILGIEPSFEAMVM--NNGVLVGEVILVY : 168

ptilGFp : NRTFTKYPDDIA--DYVQSF---PAGFFYERNIRFEDGALVEIRSDISLED---KPHYKVEYRGFPSPGPM--QKAILGMEPSFEVVM--VSGVILRGESIMAL : 162

asulGFp : NRTFTKIVSGIP--DYFKQSF---PEGFTWERTITYEDGGFLTAHOOTSLED---CLVYKVILGNFNPADGPVM--QNKAGRWEATEIIVYE--QDGVILRGNNVMAI : 162

hcriCP : SRTFVHTAEIP--DFFKQSF---PEGFTWERTITYEDGGILTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--KKSJGGWEPCTEIVYQ--DNGVILRGNNVMAI : 162

cgigCP : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTITYEDGGVLTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--KNLSGGWEPCTEIVYQ--DNGVILRGNNVMAI : 162

cpasCP : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTITYEDGGVLTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--QKKTQGWEPSTEIVIP--RDGGILLRDTTPAL : 162

asulGFp : IKVFAKYPEIP--DFFKQSL---SDGFTWRRVSNVDGGVLTVQOTSLEKD---CIIICNIKVHGTNFPENGPM--QNKIDGWEPSTEIVIP--RDGGILLRMDVPAL : 162

cgigGFp : NKVFTDYDDIP--DFFKQSL---PEGFTWRRVSNVDGGVLTVQOTSLEGD---CIIICKIKAHGTNFPADGPVM--QKRTQGWEPSTEIVIP--RDGMLIGNNFMAI : 159

hcriGFp : NKVFAKYPKDP--DFFKQSL---PEGFTWERTIMNFDGAVCTVSNDSIQGN---CFTYHVKFSGLNFPNGPM--QKKTQGWEPNTERLFA--RDGMLIGNNFMAI : 161

aaspGFp : SIPFTKYPEDIP--DYVKQSF---PEGYTWERSMHPEDGGLCCITNSIDLIGN---CFYIDYIKFTGLNFPNGPM--QKKTQGWEPSTEIVIP--RDGVLIGEDIHHA : 165

stencP : SKVVKHPADIP--DYKKLSF---PEGFKWERVMNFDGGVWTVQDSLSLDG---CFTYKVKFIVGNFSPDGPVM--QKRTQGWEPSTEIVIP--RDGVLKGEIHHA : 165

gtenGFp : SKVVKHPADIP--DYKKLSF---PEGFKWERVMNFDGGVWTVQDSLSLDG---CFTYKVKFIVGNFSPDGPVM--QKRTQGWEPSTEIVIP--RDGVLKGEIHHA : 165

DsRed : NRCTFTKYPEDIP--DYKKLSF---PDGMSYERTFTYEDGGVATASWEISLKGN---CFEHSKSTHGVNFPADGPVM--AKKTIQWDPSEFKMTV--CDGILKGDVTAFL : 167

di.s2RFP : NRCTFTKYPEDIP--DYFKQSF---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

amaJGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

zoanYFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

zoan2RFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

rflorFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

rflorFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

dis3GFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

scubGFp1 : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

scubGFp2 : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

mcavRFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

mcavGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

dendGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

clavGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

GFp : VQFSRYPDHMKQHDFFKSAM---PEGVQERTIFYKDDGNYKRAEVKFGD---TVNRIELKGDIFKEDGNILGHKMEYNNSHVYTNADKQNGIKVNFKIRH : 169

irmulGFp : NRTFTKYPNDIS--DYFIQSF---PAGFWERILRYEDGGLVEIRSDINLIED---KFVVRVEYKGSNFPDDGPVM--QKTIILGIEPSFEAMVM--NNGVLVGEVILVY : 168

ptilGFp : NRTFTKYPDDIA--DYVQSF---PAGFFYERNIRFEDGALVEIRSDISLED---KPHYKVEYRGFPSPGPM--QKAILGMEPSFEVVM--VSGVILRGESIMAL : 162

asulGFp : NRTFTKIVSGIP--DYFKQSF---PEGFTWERTITYEDGGFLTAHOOTSLED---CLVYKVILGNFNPADGPVM--QNKAGRWEATEIIVYE--QDGVILRGNNVMAI : 162

hcriCP : SRTFVHTAEIP--DFFKQSF---PEGFTWERTITYEDGGILTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--KKSJGGWEPCTEIVYQ--DNGVILRGNNVMAI : 162

cgigCP : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTITYEDGGVLTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--KNLSGGWEPCTEIVYQ--DNGVILRGNNVMAI : 162

cpasCP : SKTFIKHTSGIP--DYFKQSF---PEGFTWERTITYEDGGVLTAHOOTSLEGN---CLIVYKVLGINTFPADGPVM--QKKTQGWEPSTEIVIP--RDGGILLRDTTPAL : 162

asulGFp : IKVFAKYPEIP--DFFKQSL---SDGFTWRRVSNVDGGVLTVQOTSLEKD---CIIICNIKVHGTNFPENGPM--QNKIDGWEPSTEIVIP--RDGGILLRMDVPAL : 162

cgigGFp : NKVFTDYDDIP--DFFKQSL---PEGFTWRRVSNVDGGVLTVQOTSLEGD---CIIICKIKAHGTNFPADGPVM--QKRTQGWEPSTEIVIP--RDGMLIGNNFMAI : 159

hcriGFp : NKVFAKYPKDP--DFFKQSL---PEGFTWERTIMNFDGAVCTVSNDSIQGN---CFTYHVKFSGLNFPNGPM--QKKTQGWEPNTERLFA--RDGMLIGNNFMAI : 161

aaspGFp : SIPFTKYPEDIP--DYVKQSF---PEGYTWERSMHPEDGGLCCITNSIDLIGN---CFYIDYIKFTGLNFPNGPM--QKKTQGWEPSTEIVIP--RDGVLIGEDIHHA : 165

stencP : SKVVKHPADIP--DYKKLSF---PEGFKWERVMNFDGGVWTVQDSLSLDG---CFTYKVKFIVGNFSPDGPVM--QKRTQGWEPSTEIVIP--RDGVLKGEIHHA : 165

gtenGFp : SKVVKHPADIP--DYKKLSF---PEGFKWERVMNFDGGVWTVQDSLSLDG---CFTYKVKFIVGNFSPDGPVM--QKRTQGWEPSTEIVIP--RDGVLKGEIHHA : 165

DsRed : NRCTFTKYPEDIP--DYKKLSF---PDGMSYERTFTYEDGGVATASWEISLKGN---CFEHSKSTHGVNFPADGPVM--AKKTIQWDPSEFKMTV--CDGILKGDVTAFL : 167

di.s2RFP : NRCTFTKYPEDIP--DYFKQSF---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

amaJGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

zoanYFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

zoan2RFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

rflorFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

rflorFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

dis3GFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

scubGFp1 : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

scubGFp2 : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

mcavRFP : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

mcavGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

dendGFp : NRCTFTKYPEDIP--DYFKNSC---PAGYTWDRSFLFEDGAVCIQVADITVSVE--ENQWYHSEKFGVNFADGPVM--KMTIDNWPESCEKIIIPVKQGIILKGDVSMYL : 169

clavGF

FIG. 7C

	170	180	190	200	210	220	230	
GFP	: NIEDG-SVQLADHYQONTPIGDG-PVLLPDNHYLSTQSALS	KDOPNEKRDMILLEFVTAAGITHGMDELYK-----	: 238					
rmulGFP	: KLANG-KYYSCHMKITLMSKGV--VKEFPYVHFIOHRLEKTYVEDGG--FVEQHETAIAQMTSIGKPLGSLHEWV-----	: 238						
ptilGFP	: KLESG-NYYSCHMKITFYRSKGG--VKEFPYVHFIOHRLEKTYVEEGS--FVEQHETAIAQMTSIGKPLGSLHEWV-----	: 238						
asulGFP	: KCPGG-RHLTCHLHTTYRSKPKASALKMPGFHEDHRIEIMEEVEKKG-CYKQYEAAGRYCDAAPS	KLGHN-----	: 232					
hcriCP	: KVGDR--RLI CHLTYSYRSKKAVALTMPGFHFDIRLQMPRKKOE--YFELYEASVARYSDLPEKAN-----	: 227						
cgigCP	: KVSGR-PPLI CHLHSTVRSKK-ACALTMPGFHFDALRIOMP	KKKOE--YFELYEASVARYSDVPEKAT-----	: 227					
cpasCP	: KVSGR-PPLI CHLHSTVRSKK-ACALTMPGFHFDALRIOMP	KKKOE--YFELYEASVARYSDLPEKAN-----	: 227					
asulGFP	: MLADG-GHLSCFMETTYKSKK---EVKLPELHFFHLRMEKLSVSDDGK-TVEQHESVASYSQVPSKLGHN-----	: 228						
cgigGFP	: RLDRK-GHLI CHMETTYKPNK---EVKLPELHFFHLRMEKLSVSDDGK-TI KOHEYVVASYSKVPSKIGROW-----	: 229						
hcriGFP	: KLEGG-GHLLCVMETTYKSKK---KVNLPKPHFHLRMEKOSVSDDEK-TIEQHENVRASVYFNDSGK-----	: 225						
asp?FP	: KLEGG-GHVLCEFKSTVYKAKK---PVRMPGYHYVDRKLDVTNNKDYT-SVEQCEISIARKPVVA-----	: 219						
gtenCP	: KLEGG-GHVLCEFKSTVYKAKK---PVRMPGYHYVDRKLDVTNNIDYT-SVEQCEISIARKPVVA-----	: 221						
dstrGFP	: TVEGG-GHYACDIKTVYRAKKA---ALKMPGYHYVDTKLVIWNNDEKFM-KVEEHELAVARHPFYEPKDK-----	: 232						
DsRed	: KLDG-GHYLVEFKSIYMAKK---PVQLPGYVYVDSKLDITSHNEDYT-IVEQYERTEGRHHLFL-----	: 225						
dis2RFP	: RLEGG-GHYLVEFKSIYMAKK---PSVQLPGYVYVDSKLDITSHNEDYT-IVEQYERTEGRHHPFTIKPL-----	: 229						
amajGFP	: MLQGG-GNYRCQFHTSYTKKK---FVTMPNHHVVEHRIARTDLDKGN-SVQLTEHAVAHITSVF-PF-----	: 229						
zoanGFP	: LLDKG-GRLCQFDTVYKAKSV--PRIMPDPWHFIOHKLITREDRSDAKNQKWLTEHAIAAGSALP-----	: 231						
zoanYFP	: LLDKG-GRYRCQFDTVYKAKSV--PSKMPDWHFIOHKLITREDRSDAKNQKWLTEHAIAFPSALA-----	: 231						
zoan2RFP	: LLDKG-GRYRCQFDTIYKAKTE--PKEMPDWHFIOHKLITREDRSDAKNQKWLTIEHAIASRSALP-----	: 231						
rflorFP	: LLDKG-GRYRCQFDTIYKPKK---NVKMPGYHFDHCHIEITSQQDDYN-WVELYEGAVAHYSPLQPCQAKA-----	: 231						
rflorGFP	: LLDKG-GRYRCQFDTIYTPKR---KVNMPGYHFDHCHIEIQKHDKDYN-MAVLEDAVAHNSPLEKKSQAKA-----	: 231						
dis3GFP	: LLDKG-GRYRCQFDTIYKPNK---VVRMPDYHFDHYTIEITSQQNYN-WVELTEVAEAFARYSSLEKIGSKA-----	: 234						
scubGFP1	: LLDKG-GRYRCQFDTIYKAKNVP--HPPGYHYVVDHCHIEILEERKDH---VKLREHAKARSLSPTSASAKERKA-----	: 235						
scubGFP2	: LLDKG-GRYRCQFDTIYKAKNVPPTALPDYHYVVDHCHIEILEERKDY--VNLQYAKARSGLHLPELQK-----	: 235						
mcavRFP	: LLDKG-GRYRCQFDTIYRAKKK--GVKLPDYHFDHCHIEILRHDKET--EVKLYEHAHSGSLPRGQKA-----	: 227						
mcavGFP	: LLDKG-GRYRCQFDTIYKAKK---VVRLPDYHFDHCHIEILRHDKDYN-KVKLHEHAHSGSLPRGQKA-----	: 234						
dendGFP	: LLDKG-GRYRCQFDTIYKAKK---VVRLPDYHFDHCHIEILRHDKDYN-KVKLHEHGVARYSPLPKSLVEVQKAITMA-----	: 236						
clavGFP	: LLDKG-GRYRCQFDTIYKAKK---VVKLPDYHFDHCHIEILRHDKDYN-KVTLYENAVARYSILL--PSQA-----	: 266						

E a
P h
v k
c

c y k p h E a

FIG. 8

Green fluorescent protein from *Heteractis crispa* hcrGFP

```

10      20      30      40      50      60
ATTTTGGACAGGTGTTCAACCAAGCAAATTTAAGAAGTCATCATCTTTATCTCAGTCAGG

70      80      90      100     110     120
AAAATGTGTTCTTACATCAAAGAAACCATGCAAAGTAAGGTTTACATGGAAGGAAAAGTT
M C S Y I K E T M Q S K V Y M E G K V

130     140     150     160     170     180
AACGACCACAACCTTCAAGTGCACTGCAGAAGGAAAAGGAGAACCATACAAAGGCTCACAA
N D H N F K C T A E G K G E P Y K G S Q

190     200     210     220     230     240
AGCCTGACGATCACCGTAACTGAAGGAGGTCTCTGCCATTTGCCTTCGACATTCTTTCA
S L T I T V T E G G P L P F A F D I L S

250     260     270     280     290     300
CACGCCTTTTCGATATGGCAATAAGGTGTTTCGCCAAGTACCCCAAAGATCATCTGATTTT
H A F R Y G N K V F A K Y P K D H P D F

310     320     330     340     350     360
TTTAAGCAGTCTCTTCCTGAAGGTTTTACTTGGGAAAGAGTAAGCAACTATGAGGACGGA
F K Q S L P E G F T W E R V S N Y E D G

370     380     390     400     410     420
GGAGTCCTTACCGTTAAACAAGAACTAGTCTGGAGGGAGATTGCATTATTTGCAAAATT
G V L T V K Q E T S L E G D C I I C K I

430     440     450     460     470     480
AAAGCACATGGCACTAACTTCCCCGCAGATGGTCCGGTGATGCAAAAACGGACCAATGGA
K A H G T N F P A D G P V M Q K R T N G

490     500     510     520     530     540
TGGGAGCCATCAACTGAAACGGTTATTCCACGGGTGGAGGAATTCTGATGCGCGATGTG
W E P S T E T V I P R G G G I L M R D V

550     560     570     580     590     600
CCCGCACTGAAGCTGCTTGGTAACAAAGGACATCTTCTCTGCGTCATGGAAACAATTAC
P A L K L L G N K G H L L C V M E T T Y

610     620     630     640     650     660
AAGTCAAAAAAAAAAGGTGAACCTGCCAAACCGCACTTTTCATCATTTGAGAATGGAGAAG
K S K K K G E P A K P H F H H L R M E K

670     680     690     700     710     720
GATAGTGTTAGTGACGATGAGAAGACCATTGAGCAGCACGAGAATGTGAGGGCAAGCTAC
D S V S D D E K T I E Q H E N V R A S Y

730     740     750     760     770     780
TTCAATGATAGTGGAAAATGATCATTTCTTATTGATTTCAATGTTAGGGCATTGAGTTT
F N D S G K *

790     800     810     820     830     840
CCAAATTTTCTTAGACACAGTCTTTTCCTTTAGCTTCGTAGCCTACTTACCCATGTTTTG

850     860
TTGAAGTCAATAAATAGCTAAGCACTAC (SEQ ID NOS: 01 & 02)

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FIG. 9

Green fluorescent protein from *Dendronephthya sp.* dendGFP

```

      10      20      30      40      50      60
5' CATATCGAGAAAGTTGTGAAACCAAATTCTTACTCTACTTTTACTACCATGAATCTGATT
                                     M N L I

      70      80      90     100     110     120
AAAGAAGATATGAGGGTTAAGGTGCATATGGAAGGGAATGTAAACGGGCATGCTTTTGTG
K E D M R V K V H M E G N V N G H A F V

     130     140     150     160     170     180
ATTGAAGGGGAAGGAAAAGGAGCCCTACGAAGGGACACAGACCTTGAACCTGACAGTG
I E G E G K G R P Y E G T Q T L N L T V

     190     200     210     220     230     240
AAAGAAGGCGCGCCTCTCCCATTTTCTTACGACATCTTGACAACAGCATTGCACTACGGA
K E G A P L P F S Y D I L T T A L H Y G

     250     260     270     280     290     300
AACAGAGTATTCACTGAATACCCAGCAGATATCACGGATTATTTCAAGCAATCATTTTCT
N R V F T E Y P A D I T D Y F K Q S F P

     310     320     330     340     350     360
GAAGGATATTCCTGGGAAAGAACCATGACTTATGAAGACAAGGGCATTGTACCATCAGA
E G Y S W E R T M T Y E D K G I C T I R

     370     380     390     400     410     420
AGCGACATAAGCTTGGAAGGTGACTGCTTTTCCAAAACATTTCGTTTAAATGGGATGAAC
S D I S L E G D C F F Q N I R F N G M N

     430     440     450     460     470     480
TTTCCCCCAAATGGTCCAGTTATGCAGAAGAAAACTTTGAAGTGGAACCATCCACAGAG
F P P N G P V M Q K K T L K W E P S T E

     490     500     510     520     530     540
AAGCTGCACGTGCGTGATGGGTTGCTTGTGCGTAATATTAACATGGCTCTGCTGCTTGAA
K L H V R D G L L V G N I N M A L L L E

     550     560     570     580     590     600
GGAGGTGGACATTACCTGTGTGACTTCAAACTACTTACAAAGCGAAGAAGGTTGTTTCAG
G G G H Y L C D F K T T Y K A K K V V Q

     610     620     630     640     650     660
TTGCCAGATTATCATTTTGTGGACCATCGCATTGAGATCTTGAGTAATGACAGCGATTAC
L P D Y H F V D H R I E I L S N D S D Y

     670     680     690     700     710     720
AACAAAGTGAAGCTGTACGAGCATGGGGTTGCTCGCTATTCTCCGTTGCCCAAGTCAGGC
N K V K L Y E H G V A R Y S P L P K S G

     730     740     750     760     770     780
CTGGTAGAGGTTCAAGGGAAAGCCATAATGACTGCATAGATAAACATGTAGTGAAGACCA
L V E V Q G K A I M T A *

     790     800     810     820     830     840
CATACTCGGGATTAGAGTTTAGGGATTGGTAGTTGTGGTAGATTCTAGCCTACAAATTTT

```

TTGGG 3' (SEQ ID NO:03 & 04)

FIG. 10

Red fluorescent protein from *Zoanthus* sp. zoanRFP

```

      10      20      30      40      50      60
GAGTTGAGTTCTCGACTTCAGTTGTATCACTTTTGACGTATCAAGTGATCTATTCTCAAC

      70      80      90     100     110     120
ATGGCCCATTCAAAGCACGGACTAACAGATGACATGACAATGCATTTCCGTATGGAAGGG
M A H S K H G L T D D M T M H F R M E G

      130     140     150     160     170     180
TGGCTCGATGGACATAAGTTTGTAAATCGAGGGCAACGGCAATGGAAATCCTTTCAAAGGG
C V D G H K F V I E G N G N G N P F K G

      190     200     210     220     230     240
AAACAGTTTATTAATCTGTGTGTGATTGAAGGAGGACCACTGCCATTCTCCGAAGACATA
K Q F I N L C V I E G G P L P F S E D I

      250     260     270     280     290     300
TTGTCTGCTGCGTTTGACTIONRGLFT E Y P E G I V

      310     320     330     340     350     360
GACTATTTCAAGAACTCGTGTCTGCTGGATATACGTGGCACAGGTCTTTTCGCTTTGAA
D Y F K N S C P A G Y T W H R S F R F E

      370     380     390     400     410     420
GATGGAGCAGTTTGCATATGCAGTGCAGATATAACAGTAAATGTTAGGGAAAACCTGCATT
D G A V C I C S A D I T V N V R E N C I

      430     440     450     460     470     480
TATCATGAGTCCACGTTTATGGAGTGAACCTTTCCTGCTGATGGACCTGTGATGAAAAAG
Y H E S T F Y G V N F P A D G P V M K K

      490     500     510     520     530     540
ATGACAATAATTGGGAACCGTCCTGCGAGAAAATCATACCAATAAATAGTCAGAAGATA
M T T N W E P S C E K I I P I N S Q K I

      550     560     570     580     590     600
TTAAAAGGGGATGTCTCCATGTACCTCCTTCTGAAGGATGGTGGGCGTTACCGCTGCCAG
L K G D V S M Y L L L K D G G R Y R C Q

      610     620     630     640     650     660
TTTGACACAATTTACAAAGCAAAGACTGAGCCAAAAGAAATGCCGGACTGGCACTTCATC
F D T I Y K A K T E P K E M P D W H F I

      670     680     690     700     710     720
CAGCATAAGCTCAACCGTGAAGACCGCAGCGATGCTAAGAATCAGAAATGGCAACTGATA
Q H K L N R E D R S D A K N Q K W Q L I

      730     740     750     760     770     780
GAACATGCTATTGCATCCCGATCTGCTTTACCCCTGATAACAAAGGAGTTGCTATTGCATG
E H A I A S R S A L P *

      790     800     810     820     830     840
TGCATGCCTATTACGCTGATAAAAATGTAGTTTAAACATGCAATTGTATGTGCATGCACA

      850
TTACCCTGATA
  
```

(SEQ ID NOS:05 & 06)

FIG. 11

Green fluorescent protein from *Scolymia cubensis* scubGFP1 (AY037767)

```

      10      20      30      40      50      60
5' TGTGACATTTCAGTCATATAGGAGCCTCTATCGGAGCTGAGGTCCCATTACCGTTGTGAT
      70      80      90     100     110     120
   TTGGACGGGAGCAGATCGAGAACAACMAGGGCTGTACGAGTCTGATAATTTACTTTACAT
      130     140     150     160     170     180
   CTACCAACATGCAGCGTGCTGGGATGAAGGTTAAGGAACATATGAAGATCAAACCTGCGTA
      M   Q   R   A   G   M   K   V   K   E   H   M   K   I   K   L   R   M

      190     200     210     220     230     240
   TGGGAGGTACTGTAAACGAAAGCATTTTCGCGGTTAATGGGACAGGAGACGGCTACCCTT
      G   G   T   V   N   G   K   H   F   A   V   N   G   T   G   D   G   Y   P   Y

      250     260     270     280     290     300
   ATCAGGGAAACAGATTTTGAAACTTATCGTCGAAGGCAGCGAACCTCTGCCTTTTCGCTT
      Q   G   K   Q   I   L   K   L   I   V   E   G   S   E   P   L   P   F   A   F

      310     320     330     340     350     360
   TTGATATCTTGTTCAGCAGCATTCCAGTATGGCAACAGGGCATTACCGAATACCCAACAG
      D   I   L   S   A   A   F   Q   Y   G   N   R   A   F   T   E   Y   P   T   E

      370     380     390     400     410     420
   AGATAGCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTTCTCCTGGGAACGAA
      I   A   D   Y   F   K   Q   S   F   E   F   G   E   G   F   S   W   E   R   S

      430     440     450     460     470     480
   GTTTCACTTTCGAAGATGGGGCCATTTCGCTCGCCACCAACGATATAACGATGGTTGGTG
      F   T   F   E   D   G   A   I   C   V   A   T   N   D   I   T   M   V   G   G

      490     500     510     520     530     540
   GTGAGTTTCAGTATGATATTCGATTGATGGTCTGAACTTCCCTGAAGATGGTCCAGTGA
      E   F   Q   Y   D   I   R   F   D   G   L   N   F   P   E   D   G   P   V   M

      550     560     570     580     590     600
   TGCAAAAGAAAACCGTAAATGGGAGCCATCCACTGAGATAATGTATATGCAAAATGGAG
      Q   K   K   T   V   K   W   E   P   S   T   E   I   M   Y   M   Q   N   G   V

      610     620     630     640     650     660
   TGCTGAAGGGTGAGGTTAACATGGCTCTGTTGCTTCAAGACAAAAGCCATTACCGTTGCG
      L   K   G   E   V   N   M   A   L   L   L   Q   D   K   S   H   Y   R   C   D

      670     680     690     700     710     720
   ACCTCAAAACTACTTACAAAGCTAAGAATAATGTGCCGCATCCTCCAGGCTACCACTATG
      L   K   T   T   Y   K   A   K   N   N   V   P   H   P   P   G   Y   H   Y   V

      730     740     750     760     770     780
   TGGATCACTGCATTGAAATACTCGAAGAACGTAAGGATCACGTTAAGCTGCGGGAGCATG
      D   H   C   I   E   I   L   E   E   R   K   D   H   V   K   L   R   E   H   A

      790     800     810     820     830     840
   CTAAAGCTCGTTCTAGCCTGTACCTACCAGTGCAAAAGAACGAAAGGCTTAGGTGATAG
      K   A   R   S   S   L   S   P   T   S   A   K   E   R   K   A   *

      850     860     870     880     890     900
   TCAAAAAGACAACAAGACGAAAATGAAAGGTGTTCAATTGTTAGAAATTTGATATTTTCGAT
      910     920     930     940     950     960
   TCAATGATTTCGTTAAGGGATTGCTAGAGGCTAGCTAACAGGTTAACATCATAAGGATAG
      970     980     990     1000    1010    1020
   AGATTTCGTTGCGGAGTTAGAACCTTTWATATTTTCCGAATTCCAMCTAGAGTCGTTGAGA
      1030    1040    1050    1060    1070    1080
   AATTTATTAGAGACTAGCTTTAGAGTTACTTTTGTGGAAAAAAGGTTTCCATTTTTTGC
      1090    1100    1110    1120    1130    1140
   GTTATTACAGCATTTAAAGCATAGGAATAGAGATTTCGGTTATGGAAAATAACAGTAGGAA
      1150    1160    1170
   AATACGTTGTGAAAATAAACTTGTGTGTCGAAAAA 3'

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(SEQ ID NOS:07&08)

FIG. 12

Green fluorescent protein from *Scolymia cubensis* scubGFP2 (AY037771)

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      10      20      30      40      50      60
5' CCTGGTGATTTGGACGAGAGCAGATCGAGAATAGCAAGGTTTACCAGCGTGATAATTTA
      70      80      90     100     110     120
   CTTTACATCTAACAACATGCAATCTGCTGGGAAGAAGAATGTCGTTAAGGACTTCATGAA
           M  Q  S  A  G  K  K  N  V  V  K  D  F  M  K

      130     140     150     160     170     180
   GATCACACTGCGTATGGACGGTGCTGTAAACGGGAAGCCCTTCGCGGTTAATGGAACAGG
   I  T  L  R  M  D  G  A  V  N  G  K  P  F  A  V  N  G  T  G

      190     200     210     220     230     240
   AGATGGCAACCCTTATGGTGAATACAGAGTTTGAAGCTTACCGTCGATGGCAACAAACC
   D  G  N  P  Y  G  G  I  Q  S  L  K  L  T  V  D  G  N  K  P

      250     260     270     280     290     300
   TCTGCCTTTTGTCTTTTGATATCTTGTTCAGCAGCATTCCAGTATGGCAACAGGGCATTAC
   L  P  F  A  F  D  I  L  S  A  A  F  Q  Y  G  N  R  A  F  T

      310     320     330     340     350     360
   CGAATACCCAAAAGAGATATCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTT
   E  Y  P  K  E  I  S  D  Y  F  K  Q  S  F  E  F  G  E  G  F

      370     380     390     400     410     420
   TACCTGGGAACGAAGTTTCACTTTTCAAGACGGGGCCATTTCGTCGCCACGAACGATAT
   T  W  E  R  S  F  T  F  E  D  G  A  I  C  V  A  T  N  D  I

      430     440     450     460     470     480
   AAAGATGGTTGGCGATGAGTTTCAATATAACATTCCGATTTGATGGTGTGAATTTCCCTGA
   K  M  V  G  D  E  F  Q  Y  N  I  R  F  D  G  V  N  F  P  E

      490     500     510     520     530     540
   AGATGGTCCWGTATGCAGAAGAAAACGGTGAAGTGGGAGCCATCCACAGAGATAATGCG
   D  G  P  V  M  Q  K  K  T  V  K  W  E  P  S  T  E  I  M  R

      550     560     570     580     590     600
   TGTGCAAGGTGGAGTGCTAAAGGGTGAGGTTAACATGGCTCTGTTGCTTAAAGACAAAAG
   V  Q  G  G  V  L  K  G  E  V  N  M  A  L  L  L  K  D  K  S

      610     620     630     640     650     660
   CCATTACCGATGTGACTTCAAACTACTTTACAAAGCTAAGAATCCTGTCCCGCCGACGGC
   H  Y  R  C  D  F  K  T  T  Y  K  A  K  N  P  V  P  P  T  A

      670     680     690     700     710     720
   GCTTCCAGACTACCACTATGTGGATCACTGTATTGAAATCACCGAGGAAAATAGGGATTA
   L  P  D  Y  H  Y  V  D  H  C  I  E  I  T  E  E  N  R  D  Y

      730     740     750     760     770     780
   CGTTAAGCTGCAGGAGTATGCTAAAGCTCGTTCTGGCCTGCACCTGCCCGAACTGCAAAA
   V  K  L  Q  E  Y  A  K  A  R  S  G  L  H  L  P  E  L  Q  K

      790     800     810
   GTAAAGGCTTAGGCGATAGTCAAGACGACAACGAGAAGA 3'
   *
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(SEQ ID NO:09 & 10)

FIG. 13

Red fluorescent protein from *Ricordea florida* rflorFP (AY037773)

```

      10      20      30      40      50      60
5'TGTGAAAGTTAACATTTTACTTTACTTCTACCAGCATGAGTGCACTCAAAGAGGAAATGA
      M   S   A   L   K   E   E   M   K

      70      80      90     100     110     120
AAATCAAGCTTACATTGGTGGGCGTTGTTAACGGGCACCCATTCAAGATCATTGGGGACG
   I   K   L   T   L   V   G   V   V   N   G   H   P   F   K   I   I   G   D   G

     130     140     150     160     170     180
GAAAGGCAAACCTATGAGGGATCGCAGGAATTAACCCCTTGCCGTGGTGAAGGAGGGC
   K   G   K   P   Y   E   G   S   Q   E   L   T   L   A   V   V   E   G   G   P

     190     200     210     220     230     240
CTCTGCCTTTCTCTTATGATATCCTGACAACGATAGTTCACTATGGCAACAGGGCATTG
   L   P   F   S   Y   D   I   L   T   T   I   V   H   Y   G   N   R   A   F   V

     250     260     270     280     290     300
TGAATAACCAAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGGTGCTG
   N   Y   P   K   D   I   P   D   I   F   K   Q   T   C   S   G   P   G   A   G

     310     320     330     340     350     360
GATATTCCTGGCAAAGGACCATGAGTTTGAAGACGGAGGCGTTTGCCTGCTACGAGCC
   Y   S   W   Q   R   T   M   S   F   E   D   G   G   V   C   T   A   T   S   H

     370     380     390     400     410     420
ATATCAGGGTGGATGGCGACACTTTCAATTATGACATTCACTTCATGGGAGCGGATTTC
   I   R   V   D   G   D   T   F   N   Y   D   I   H   F   M   G   A   D   F   P

     430     440     450     460     470     480
CTCTTAATGGTCCAGTGATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAA
   L   N   G   P   V   M   Q   K   R   T   V   K   W   E   P   S   T   E   I   M

     490     500     510     520     530     540
TGTTTCAATGTGATGGATTGCTGAGGGGTGATGTTGCCATGTCTCTGTTGCTGAAAGGAG
   F   Q   C   D   G   L   L   R   G   D   V   A   M   S   L   L   L   K   G   G

     550     560     570     580     590     600
GCGGCCATTACCGATGTGACTTTAAACTATTTATAAACCCCAAGAAGAATGTCAAGATGC
   G   H   Y   R   C   D   F   K   T   I   Y   K   P   K   K   N   V   K   M   P

     610     620     630     640     650     660
CAGGTTACCATTTTGTGGACCACTGCATTGAGATAACGAGTCAACAGGACGATTACAACG
   G   Y   H   F   V   D   H   C   I   E   I   T   S   Q   Q   D   D   Y   N   V

     670     680     690     700     710     720
TGTTTGAGCTGTACGAGGGTGCTGTAGCCCACTACTCTCCTCTGCAGAAACCATGCCAAG
   V   E   L   Y   E   G   A   V   A   H   Y   S   P   L   Q   K   P   C   Q   A

     730     740     750     760     770     780
CAAAGGCATAAAGCCAAACAACCCAAGAGGACAACAAGACATTTAATCAAATCACATCTT
   K   A   *

     790     800
TGTATTTTGGTTAGAGTTGAAAAAAA 3'

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(SEQ ID NO:11 & 12)

FIG. 14

Green fluorescent protein from *Ricordea florida* rfloGFP (AY037772)

```

      10      20      30      40      50      60
5' AGTCACCTCGGTGTTTTTAGGACAGGAAGGATCACGAGCAAGAGAAGAACTGTGAAAGTT
      70      80      90     100     110     120
  AACACTTTACTCTACTTCTACCAGCATGAGTGCCTCAAAGAGGAAATGAAAATCAAGCT
                        M S A L K E E M K I K L

      130     140     150     160     170     180
TAAAATGGTGGGCGTTGTTAACGGGCAGTCATTTTCAGATCGATGGGGAAGGAAAAGGCAA
  K M V G V V N G Q S F Q I D G E G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGAAATTAACCCTTGAAGTGGTGAAGGAGGGCCTCTGCTCTT
  P Y E G S Q K L T L E V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTTCAGTATGGCAACAGGGCATTCTGTAACCTACC
  S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGATGGTGGATTTTCCTG
  K D I P D I F K Q T C S G P D G G F S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAAGACGGAGGGGTTTGCCTGCTTCAAACCACATCAGCGT
  Q R T M T Y E D G G V C T A S N H I S V

      430     440     450     460     470     480
GGACGGCGACACTTTTTATTATGTGATAAGATTTAATGGAGAGAATTTTCTCCAAATGG
  D G D T F Y Y V I R F N G E N F P P N G

      490     500     510     520     530     540
TCCAGTAATGCAGAAAAGAACAGTGAATGGGAGCCATCCACTGAGATAATGTTTGAACG
  P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGACATTGCCATGTCTCTGTGCTGAAAGGAGGCGGCCATTA
  D G L L R G D I A M S L L L K G G G H Y

      610     620     630     640     650     660
CCGATGTGACTTTTAAACTATTTATACACCCAAGAGGAAGGTCAACATGCCAGGTTACCA
  R C D F K T I Y T P K R K V N M P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATACAGAAGCAGACAGGATTACAACATGGCTGTGCT
  F V D H C I E I Q K H D K D Y N M A V L

      730     740     750     760     770     780
CTCTGAGGATGCTGTAGCCCACAACCTCTCCTCTGGAGAAAAAAGCCAAGCAAAGGCGTA
  S E D A V A H N S P L E K K S Q A K A *

      790
AAGCCAAACAACCTAA 3'

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(SEQ ID NO:13&14)

FIG. 15

Red fluorescent protein from *Montastraea cavernosa* mcavRFP (AY037770)

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      10      20      30      40      50      60
5'ACGCAGGGATTCAACCCTGGTGATTTGGAAGAGAGCAGACCGAGAACAACAAGAGCTGTAT
      70      80      90     100     110     120
AAGGCTGATATCTTACTTTACGTCTACCATCATGAGTGTGATTAAATCAGTCATGAAGAT
R  L  I  S  Y  F  T  S  T  I  M  S  V  I  K  S  V  M  K  I

      130     140     150     160     170     180
CAAGCTGCGTATGGAAGGCAGTGTAACGGGCACAACCTTCGTAATTGTTGGAGAAGGAGA
K  L  R  M  E  G  S  V  N  G  H  N  F  V  I  V  G  E  G  E

      190     200     210     220     230     240
AGGCAAGCCTTATGAGGGAACACAGAGTATGGACCTTACAGTCAAAGAAGGCGCACCTCT
G  K  P  Y  E  G  T  Q  S  M  D  L  T  V  K  E  G  A  P  L

      250     260     270     280     290     300
GCCTTTTCGCTACGATATCATGACAACAGTATTCCATTACGGCAATAGGGTATTTCGCAA
P  F  A  Y  D  I  M  T  T  V  F  H  Y  G  N  R  V  F  A  K

      310     320     330     340     350     360
ATACCCAAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGGAGTATTCCTGGGA
Y  P  K  H  I  P  D  Y  F  K  Q  M  F  P  E  E  Y  S  W  E

      370     380     390     400     410     420
ACGAAGCATGAATTTTCGAAGGCGGGGGCATTTCACCGCCAGGAACGAGATAACAATGGA
R  S  M  N  F  E  G  G  G  I  C  T  A  R  N  E  I  T  M  E

      430     440     450     460     470     480
AGGCGACTGTTTTTTCAATAAAGTTTCGATTTGATGGTGTGAACTTCCCCCCTAATGGTCC
G  D  C  F  F  N  K  V  R  F  D  G  V  N  F  P  P  N  G  P

      490     500     510     520     530     540
AGTCATGCAGAAGAAGACGCTGAAATGGGAGCCATCCACTGAAAAAATGTATGTGCGTGA
V  M  Q  K  K  T  L  K  W  E  P  S  T  E  K  M  Y  V  R  D

      550     560     570     580     590     600
TGGAGTGCTGACGGGTGATATCAACATGGCTTTGTTGCTTGAAGGAGGTGGCCATTACCG
G  V  L  T  G  D  I  N  M  A  L  L  L  E  G  G  G  H  Y  R

      610     620     630     640     650     660
ATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGGGTGTCAAGTTACCAGATTATCA
C  D  F  R  T  T  Y  R  A  K  K  K  G  V  K  L  P  D  Y  H

      670     680     690     700     710     720
CTTTGAGGATCACTCCATTGAGATTTTGCGCCATGACAAAGAATACTAGGTTAAGCT
F  E  D  H  S  I  E  I  L  R  H  D  K  E  Y  T  E  V  K  L

      730     740     750     760     770     780
GTATGAGCATGCCGAAGCTCATTCTGGGCTGCCGAGGGTGGCAAAGTAAAGGCTTAACGA
Y  E  H  A  E  A  H  S  G  L  P  R  V  A  K  *

      790
AAAGCCAAGACCACA 3'

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(SEQ ID NO:15 & 16)

FIG. 16

Green fluorescent protein from *Montastraea cavernosa* mcavGFP (AY037769)

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      10      20      30      40      50      60
5' ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA
      70      80      90     100     110     120
   TCTTACTTACGTCTACCATCATGACAAGTGTTCACAGGAAAAGGGTGTGATTAAACCAG
           M T S V A Q E K G V I K P D

      130     140     150     160     170     180
   ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG
       M K M K L R M E G A V N G H K F V V E G

      190     200     210     220     230     240
   GAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG
       D G K G K P F D G T Q T M D L T V I E G

      250     260     270     280     290     300
   GCGCACCATTTGCCTTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG
       A P L P F A Y D I L T T V F D Y G N R V

      310     320     330     340     350     360
   TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT
       F A K Y P E D I A D Y F K Q T F P E G Y

      370     380     390     400     410     420
   ACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTCATCGCCACAAACGACA
       F W E R S M T Y E D Q G I C I A T N D I

      430     440     450     460     470     480
   TAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTTCGATTGATGGTGTGA
       T M M E G V D D C F A Y K I R F D G V N

      490     500     510     520     530     540
   ACTTTCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACTG
       F P A N G P V M Q R K T L K W E P S T E

      550     560     570     580     590     600
   AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTG
       I M Y A R D G V L K G D V N M A L L L E

      610     620     630     640     650     660
   AAGGAGGTGGCCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAAGGTTGTCC
       G G G H Y R C D F K T T Y K A K K V V R

      670     680     690     700     710     720
   GGTTCGACGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT
       L P D Y H F V D H R I E I V S H D K D Y

      730     740     750     760     770     780
   ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA
       N K V K L H E H A E A R H G L S R K A K

      790     800     810     820     830     840
   AGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTTGTTA
   *

      850     860     870     880     890     900
   AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTGTTCGG
      910     920     930     940     950     960
   GGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAGATAGTTTCCAGTTTT
      970     980     990    1000    1010    1020
   TCGGGGATTACAGCATGGGGATAGACTTTTTTAAACTCAGTTGTGGTCAAATGCAAGTAAG
      1030    1040    1050    1060
   AAAACTGTAGTGAGAATAAACTTGTATCGAAGCCGAAAAAAAAA 3'
   (SEQ ID NOS: 17 & 18)

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FIG. 17

Green fluorescent protein from *Condylactis gigantea* cgigGFP (AY037776)

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      10      20      30      40      50      60
5' ACAGCTGTT CATCCACGCTCATTCAAGACGCCGTCAACTTTATTCCAGTCAGGAAAATGT
                                     M Y

      70      80      90     100     110     120
ATCCTTGGATCAAGGAAACCATGCGCAGTAAGGTTTACATGGAAGGAGATGTTAACAACC
  P W I K E T M R S K V Y M E G D V N N H

     130     140     150     160     170     180
ACGCCTTCAAGTGCACTGCAGTAGGAGAAGGAAAACCATACAAAGGCTCACAAGACCTGA
  A F K C T A V G E G K P Y K G S Q D L T

     190     200     210     220     230     240
CGATTACCGTCACTGAAGGAGGTCCTCTGCCATTTGCTTTCGACATTCTTTCACACGCCT
  I T V T E G G P L P F A F D I L S H A F

     250     260     270     280     290     300
TTCAGTATGGCAACAAGGTGTTTCACCGATTACCCCGACGATATTCTTGATTCTTTAAGC
  Q Y G N K V F T D Y P D D I P D F F K Q

     310     320     330     340     350     360
AGTCTCTCTCGGATGGTTTTACTTGGAGAAGAGTAAGCACSTATGACGATGGAGGAGTCC
  S L S D G F T W R R V S T Y D D G G V L

     370     380     390     400     410     420
TCACAGTTACCCAAGACACTAGTCTGAAGGAGATTGCATTATTTGCAACATTAAAGTCC
  T V T Q D T S L K G D C I I C N I K V H

     430     440     450     460     470     480
ATGGCACTAACTTCCCCGAAAATGGTCCGGTGATGCAAAACAAGACCGATGGATGGGAGC
  G T N F P E N G P V M Q N K T D G W E P

     490     500     510     520     530     540
CATCCAGCACTGAAACGGTTATTCCACAAGATGGAGGAATTGTTGCTGCGCGATCACCCG
  S S T E T V I P Q D G G I V A A R S P A

     550     560     570     580     590     600
CACTAAGGCTGCGTGATAAAGGTCATCTTATCTGCCACATGGAAACAACCTTACAAGCCAA
  L R L R D K G H L I C H M E T T Y K P N

     610     620     630     640     650     660
ACAAAGAGGTGAAGCTGCCAGAACTCCACTTTCATCATTGCGAATGGAAAAGCTGAGTG
  K E V K L P E L H F H H L R M E K L S V

     670     680     690     700     710     720
TTAGTGACGATGGGAAGACCATTAAGCAGCACGAGTATGTGGTGGCTAGCTACTCCAAAG
  S D D G K T I K Q H E Y V V A S Y S K V

     730     740     750     760     770     780
TGCCTTCGAAGATAGGACGTCAATGATCATTTCCCTTATTAAATATCAATGATGTGGCTT
  P S K I G R Q *

     790     800     810     820     830     840
TCAATTTTCCAAAATTTTGTAAAGACATAGGTCTTTTGGATTTTGGTAACCCCAACCTT
  850     860     870     880     890
AATTCCCAATAATTTTGTGGAAAGTCAAATAAAACCAGCCTTCCCTGGGCCTTTAA 3'

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(SEQ ID NOS: 19 & 20)

FIG. 18

Green fluorescent protein from *Agaricia fragilis* afraGFP (AY037765)

```

      10      20      30      40      50      60
5' CAAGGAAGCCAAATCTTTTACCAGAGATCTCGCGTGAAAGCAACCTATGAGTGATGGCGA
                                     M A I

      70      80      90     100     110     120
TTTCTACTCTAAAGAACGTCATCATCATCGTTATTATATACTCCTGCAGCACTTGTGCTG
S T L K N V I I I V I I Y S C S T C A V

      130     140     150     160     170     180
TTTGGTCGAATTCAAACTCTGAATCCTCTTTCACTAATGGGATTGCAGAGGAAATGAAGA
W S N S N S E S S F T N G I A E E M K T

      190     200     210     220     230     240
CTAGGGTACATTTGGAGGGTACTGTTAACGGGCACTCCTTTACAATTAAAGGCGAAGGAA
R V H L E G T V N G H S F T I K G E G R

      250     260     270     280     290     300
GAGGCTACCCTTACAAAGGAGAACAGTTTATGAGCCTTGAGGTCGTCAATGGTGCTCCTC
G Y P Y K G E Q F M S L E V V N G A P L

      310     320     330     340     350     360
TGCCGTTCTCTTTTGATATCTTGACACCAGCATTTATGTATGGCAACAGAGTGTTACCA
P F S F D I L T P A F M Y G N R V F T K

      370     380     390     400     410     420
AGTACCCACCAAACATACCAGACTATTTCAAGCAGACGTTTCCTGAAGGGTATCACTGGG
Y P P N I P D Y F K Q T F P E G Y H W E

      430     440     450     460     470     480
AAAGAAACATTCCCTTTGAAGATCAGGCCGCGTGCACGGTAACCAGCCACATAAGATTGG
R N I P F E D Q A A C T V T S H I R L E

      490     500     510     520     530     540
AAGAGGAAGAGAGGCGTTTTGTAAATAACGTCAGATTTCACTGTGTGAACTTTCCCCCTA
E E E R R F V N N V R F H C V N F P P N

      550     560     570     580     590     600
ATGGTCCAGTCATGCAGAGGAGGATACTGAAATGGGAGCCATCCACTGAGAACATTTATC
G P V M Q R R I L K W E P S T E N I Y P

      610     620     630     640     650     660
CGCGTGATGGGTTTCTGGAGGGCCATGTTGATATGACTCTTCGGGTTGAAGGAGGTGGCT
R D G F L E G H V D M T L R V E G G G Y

      670     680     690     700     710     720
ATTACCGAGCTGAGTTCAAAAGTACTTACAAAGGGAAGACCCAGTCCGCGACATGCCAG
Y R A E F K S T Y K G K T P V R D M P D

      730     740     750     760     770     780
ACTTTCACTTCATAGACCACCGCATTGAGATTACGGAGCATGACGAAGACTACACCAATG
F H F I D H R I E I T E H D E D Y T N V

      790     800     810     820     830     840
TTGAGCTGCATGACGTATCCTGGGCTCGTTACTCTATGCTGCCGACTATGTAAGCGGAAA
E L H D V S W A R Y S M L P T M

      850     860     870     880     890     900
AGGCAAGGCAACAAGACGCAAAACCGCCCTGTTTGTCTCTTTTCATAAGAGATTTGACAA
910     920     930     940     950     960
CCGTGGTTCTTTGCCATTTAATTTGAATTAGTTTAAATTAAATCTTTGGGATTGATGTAG
970     980     990    1000    1010    1020
ACGCTTTGGTTGCTAAGTAAGAAAACATTTGTGATTATTAAATTTGTTGCCTGAAGCAAA
1030
AAAAAAAAAA 3'

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(SEQ ID NOS:21 & 22)

FIG. 19

Green fluorescent protein from *Ricordea florida* rflGFP2 (AY037774)

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      10      20      30      40      50      60
5' AGCCACTTCGGTGTCTTGTTCGAGAGGAAGGATCACGAACAAGAGAAGCTGTAAAAGTT
      70      80      90     100     110     120
    AAAATTTTACTTTTACTTCTTCCAGCATGAATGCACTTCAAGAGGAAATGAAAATCAAGCT
                        M N A L Q E E M K I K L

      130     140     150     160     170     180
    TACAATGGTGGGCGTTGTTAACGGGCAGTCATTTAAGATCGATGGGAAAGGAAAAGGGAA
    T M V G V V N G Q S F K I D G K G K G K

      190     200     210     220     230     240
    ACCTTACGAGGGATCACAGGAATTGACCCTTAAAGTGGTGGAAAGCGGGCCTCTGCTCTT
    P Y E G S Q E L T L K V V E G G P L L F

      250     260     270     280     290     300
    CTCTTATGATATCCTGACAACGATATTTTCAGTATGGCAACAGGGCATTCGTGAAC TACC
    S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
    AAAGGACATACCAGATATTTTCAAGCAAACGTGTTCTGGTCTTGATGGCGGATATTCGTG
    K D I P D I F K Q T C S G L D G G Y S W

      370     380     390     400     410     420
    GCAAAGGACCATGACTTATGAGGACGGAGGGGTTTGTACTGCTACAAGCAACGTCAGCGT
    Q R T M T Y E D G G V C T A T S N V S V

      430     440     450     460     470     480
    GGTCCGGCGACACTTTTCAATTATGAAATTCAC TTTATGGGGGCGAATTTTCTCCAAATGG
    V G D T F N Y E I H F M G A N F P P N G

      490     500     510     520     530     540
    TCCRGTGATGCAGAAAAGAACAGTGAAGTGGGAGCCCTCCACTGAGATAATGTTTGAACG
    P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
    TGATGGATTGCTGAGGGGTGATGTTCCCATGTCTCTGTTGCTGAAAGGAGGCGACCATTA
    D G L L R G D V P M S L L L K G G D H Y

      610     620     630     640     650     660
    CCGATGTGACTTTAAACTATTTATAAACCCAACAAGAAGGTCAAGCTGCCAGGTTACCA
    R C D F K T I Y K P N K K V K L P G Y H

      670     680     690     700     710     720
    TTTTGTGGACCACTGCATTGAGATAAAGAGTCAAGAGAATGATTACAACATGGTTGCGCT
    F V D H C I E I K S Q E N D Y N M V A L

      730     740     750     760     770     780
    CTTTGAGGATGCTGTAGCACACTACTCTCTCTGGAGAAAAAGAGCCAGGCAAAGGCGTA
    F E D A V A H Y S P L E K K S Q A K A *

      790     800     810     820     830     840
    AATCCAAACAACCTAAGAAGACGACAAGGCATTCAATCTAATCGCATGTTTGAATTTTGTG
    850     860     870     880     890     900
    GTTAGGAATGTGTTGGGTGAGACTAGGTCTAGAACGTTTCATTTTGGCTGGATTTGTTTT
    910     920     930     940     950     960
    ACTCAGTTATAGACAAGAAAAAATCTTAAATGACTTGGGTTGGATTTAGCTTTTCGGCAC
    970     980     990    1000    1010    1020
    TGTCAATTCGGGATTCCTTAGAAATATTTGAGACCAAGCCTTTTTTTTGAGCTGAGAACGT
    AATC 3'
  
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(SEQ ID NOS: 23 & 24)

FIG. 20

Green fluorescent protein from *Montastraea cavernosa* mcavGFP2 (AY037768)

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10      20      30      40      50      60
5' AGAGCTGTAGGGTGATATCTTACTTACGTCTACCATCATGACCAAGTGTTGCACAGGAAAA
      M T S V A Q E K

70      80      90      100     110     120
GGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCA
G V I K P D M K M K L R M E G A V N G H

130     140     150     160     170     180
CAAGTTCGTGATTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGA
K F V I E G D G K G K P F D G T Q T M D

190     200     210     220     230     240
CCTTACAGTCATAGAAGGCGCACCATTCCTTTCGCTTACGCTATCTTGACAACAGTATT
L T V I E G A P L P F A Y A I L T T V F

250     260     270     280     290     300
CGATTACGGCAACAGGGTATTTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCA
D Y G N R V F A K Y P E D I A D Y F K Q

310     320     330     340     350     360
GACATTTCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTG
T F P E G Y F W E R S M T Y E D Q G I C

370     380     390     400     410     420
CATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTGTCTATAAAAT
I A T N D I T M M K G V D D C F V Y K I

430     440     450     460     470     480
TCGATTTGATGGTGTGAACCTTCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAA
R F D G V N F P A N G P V M Q R K T L K

490     500     510     520     530     540
ATGGGAGCCATCCACTGAGAAAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAA
W E P S T E K M Y A R D G V L K G D V N

550     560     570     580     590     600
CATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAG
M A L L L E G G G H Y R C D F K T T Y R

610     620     630     640     650     660
AGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTGGACCATCGCATTGAGATTGT
A K K V V Q L P D Y H F V D H R I E I V

670     680     690     700     710     720
GAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGG
S H D K D Y N K V K L Y E H A E A H S G

730     740     750     760     770     780
GCTGCCGAGGCAGGCCAAGTAAAGGCTTAATGAAAAGCCAAGACGACAACAAGGAGAAAC
L P R Q A K *

790     800     810     820     830     840
AAAGTATTTTTTTTGTAAATTTCAAGGCATTTACTCGGAATTAGTATTTGATACTTTTCG
850     860     870     880     890     900
ATTCAAGGATTTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTTGTATTTTGTGAAAA
910
AAAGATAGTTTCC 3'

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(SEQ ID NOS: 25 & 26)

FIG. 21

Green fluorescent protein homolog from *Montastraea annularis* mannFP (AY037766)

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      10      20      30      40      50      60
5' TGGTTAACGCAGAGTCGCGGGGGTTCTTGGCTAATAATTGATTCTATTTTGGGTGTGAC
      70      80      90     100     110     120
   ATTCAGGTTTAAAGCAGCATCCTCAGTGCTGAGGTCTCATTACCCCTGGTGATTTGGAAG
      130     140     150     160     170     180
   AGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAAAATCTTACTTGCCCTCTACCACC
      190     200     210     220     230     240
   ATGAGTATGATTAAACCAGAAATGAAGATCAAGATGCGTATGGACGGTGCTGTAAACGGG
   M S M I K P E M K I K M R M D G A V N G

      250     260     270     280     290     300
   CACAAGTTCGTGATTACAGGGGAAGGAAGCGGCGAGCCTTTTCGAGGGAAAACAGACTATG
   H K F V I T G E G S G E P F E G K Q T M

      310     320     330     340     350     360
   AACCTGACAGTCATAGACGGCGGACCTCTGCCTTTTCGCTTTTCGACATCTTGACAACAGCA
   N L T V I D G G P L P F A F D I L T T A

      370     380     390     400     410     420
   TTCGATTACGGCAMCAGGGTATTTCGCCAAATACCCAGAAGACATCCCAGACTATTTCAAG
   F D Y G X R V F A K Y P E D I P D Y F K

      430     440     450     460     470     480
   CAGTCGTTTCTTGAGGGGTTTTCTTGGGAACGAAGCATGACTTACGAAGACGGGGGCATT
   Q S F P E G F S W E R S M T Y E D G G I

      490     500     510     520     530     540
   TGCATCGCCACAAATGACATAAAAATGGAAGGCGACTGCTTTTCTTATGAAATTCGATTT
   C I A T N D I K M E G D C F S Y E I R F

      550     560     570     580     590     600
   GATGGGGTGAACTTTCTTGCCAATAGTCCAGTTATGCAGAAGAAGACCGTGAAATGGGAG
   D G V N F P A N S P V M Q K K T V K W E

      610     620     630     640     650     660
   CCATGCACTGRGGAATGTATGTGCGTGATGGAGTGCTTAAAGGTGGTCTTAACATGGCT
   P C T X E M Y V R D G V L K G G L N M A

      670     680     690     700     710     720
   CTGTTGCTTGAAGGAGGTGGCCATTTCCGATGTGACTTGAAAACCTACTTACAAAGCTAAG
   L L L E G G G H F R C D L K T T Y K A K

      730     740     750     760     770     780
   AAGGTTGTCCAGATGCCAGACTATCACTTTGTGAATCACCGACTTGAGATAACATGGCAT
   K V V Q M P D Y H F V N H R L E I T W H

      790     800     810     820     830     840
   GACGAGGATTACAACAATGTTAAGCTGTCTGAGCATGCAGAAGCTCATTCTGGACTGCCA
   D E D Y N N V K L S E H A E A H S G L P

      850     860     870     880     890     900
   AGGCAGGCCAAATAAAGGCTTGACGAAAAGCCAAAACGGCAAAGAGTACAAGAAAGTATA
   R Q A K *

      910     920     930     940     950     960
   TATAAATGTATATTTTTCAACTGAAAGGCATTCCACTCGGAATTAGTATTTGATACTTTT
      970     980     990    1000    1010    1020
   AATTCAAGGATTTATTTTGGGATTTGCTAGCCACTAGCTTTATTGTTAAATTAAGTTAAA
      1030    1040    1050    1060    1070    1080
   GACGGTTTAGCATTTTTCGGTATTACAACATAGGCACAGACGTCTTAACCCAGTAGTG
      1090    1100    1110    1120    1130
   GTCAGGTACAAGTAAGAAAACCTTGGTGAGAATAGACTTGTAGTCGAAAAAAA 3'

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(SEQ ID NOS:27 & 28)